What is claimed:

1. A method for producing a B6 vitamer comprising culturing an organism with an increased YaaD and/or YaaE activity as compared to the parent organism.

2. The method of claim 1, wherein increased YaaD and/or YaaE activity is due to increased expression of a nucleic acid molecule encoding a YaaD polypeptide and/or a YaaE polypeptide as compared to an unmodified parent organism.

3. The method of claim 2, wherein increased *yaaD* and/or *yaaE* nucleic acid molecule expression is due to the deregulation or introduction of nucleic acid molecules encoding a YaaD polypeptide and/or a YaaE polypeptide into the organism.

4. The method of claim 3, wherein said *yaaD* nucleic acid molecule encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:21 and/or wherein said *yaaE* nucleic acid encodes a polypeptide comprising the amino acid sequence SEQ ID NO:23.

5. The method of claim 3, wherein said *yaaD* nucleic acid encodes a polypeptide comprising an amino acid sequence which is at least 30% identical to the amino acid sequence of SEQ ID NO:21, said polypeptide having a YaaD activity.

6. The method of claim 3, wherein said *yaaE* nucleic acid encodes a polypeptide comprising an amino acid sequence which is at least 30% identical to the amino acid sequence of SEQ ID NO:23, said polypeptide having a YaaE activity.

7. The method of claim 3, wherein a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:20 and/or SEQ ID NO:22 is introduced.

8. The method of claim 1, wherein the organism is selected from the group consisting of plants and microorganisms.

9. The method of claim 8, wherein the microorganism is selected from the group consisting of algae, fungi, yeast, and bacteria.

10. A method for producing a B6 vitamer comprising culturing an organism with an increased Epd, PdxA, PdxJ, PdxF, PdxB, PdxH, and/or a Dxs activity as compared to the parent organism.

11. The method of claim 10, wherein increased Epd, PdxA, PdxJ, PdxF, PdxB, PdxH, and/or a Dxs activity is due to increased expression of a nucleic acid molecule encoding an Epd, PdxA, PdxJ, PdxF, PdxB, PdxH, and/or Dxs polypeptide as compared to an unmodified parent organism.

12. The method of claim 11, wherein increased *epd, pdxA, pdxJ, pdxF, pdxB, pdxH,* and/or *dxs* nucleic acid molecule expression is due to the introduction of nucleic acid molecules encoding an Epd, PdxA, PdxJ, PdxF, PdxB, PdxH, and/or Dxs polypeptide into the organism.

13. The method of claim 12, wherein said *pdxA* nucleic acid encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:25 and/or wherein said *pdxJ* nucleic acid encodes a polypeptide comprising the amino acid sequence SEQ ID NO:27.

14. The method of claim 12, wherein said *pdxA* nucleic acid encodes a polypeptide comprising an amino acid sequence which is at least 30% identical to the amino acid sequence of SEQ ID NO:25, said polypeptide having a PdxA activity.

15. The method of claim 12, wherein said *pdxJ* nucleic acid encodes a polypeptide comprising an amino acid sequence which is at least 30% identical to the amino acid sequence of SEQ ID NO:27, said polypeptide having a PdxJ activity.

16. The method of claim 12, wherein a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:24 and/or SEQ ID NO:26 is introduced.

17. The method of claim 10, wherein the organism is selected from the group consisting of plants and microorganisms.

18. The method of claim 17, wherein the microorganism is selected from the group consisting of algae, fungi, yeast, and bacteria.

19. An organism that has been genetically modified to comprise a recombinant DNA molecule that results in the increase of the activity of one or more enzymes that catalyze(s) a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism.

20. The organism of claim 19, wherein B6 vitamer production is at least ten-fold higher than from the unmodified parent organism.

21. The organism of claim 19, wherein said enzyme is one or more of YaaD or YaaE, or a homologue thereof, wherein said homologue has the ability to rescue an auxotroph in a test system.

22. The organism of claim 21, wherein said homologue is selected from the homologues listed in Table 9 or Table 10.

23. The organism of claim 19, wherein said organism is genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer.

24. The organism of claim 23, wherein said genes are derived from *Bacillus*.

25. The organism of claim 23, wherein said genes are derived from *Bacillus subtilis*.

26. The organism of claim 23, wherein at least one of said genes is a *yaaD* gene.

27. The organism of claim 23, wherein at least one of said genes is a *yaaE* gene.

28. The organism of claim 23, wherein at least two of said genes are *yaaD* and *yaaE* genes.

29. The organism of claim 23, wherein said organism is a *Bacillus* strain.

30. The organism of claim 23, wherein said organism is *Bacillus subtilis*.

31. The organism of claim 23, wherein said organism is *Escherichia coli*.

32. The organism of claim 19, wherein said genes are selected from the group consisting of *E. coli epd, pdxA, pdxJ, pdxF, pdxB, pdxH* or *dxs*.

33. The organism of any one of claims 19-30, wherein said organism is grown in a liquid culture and the total B6 vitamer concentration in the culture supernatant is at least 7.0 mg/liter.

34. A method of producing a B6 vitamer comprising culturing a microorganism that has been genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism, under conditions such that the B6 vitamer is produced.

35. The method of claim 34, wherein said enzyme is one or more of YaaD or YaaE.

36. The method of claim 34, wherein at least one of said genes is a *yaaD* gene.

37. The method of claim 34, wherein at least one of said genes is a *yaaE* gene.

38. The method of claim 34, wherein said genes are contained on the *yaaDE* operon.

39. The method of claim 34, wherein the B6 vitamer is pyridoxine.

40. The method of claim 34, wherein the B6 vitamer is pyridoxal.

41. The method of claim 34, wherein the B6 vitamer is pyridoxamine.

42. The method of claim 34, wherein said genes are bacterial-derived.

43. The method of claim 34, wherein said genes are derived from *Bacillus*.

44. The method of claim 34, wherein said genes are derived from *Bacillus subtilis*.

45. The method of claim 34, wherein the microorganism is Gram positive.

46. The method of claim 34, wherein the microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Cornyebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.

47. The method of claim 34, wherein the microorganism is of the genus *Bacillus*.

48. The method of claim 34, wherein the microorganism is *Bacillus subtilis*.

49. The method of claim 34, further comprising recovering the B6 vitamer.

50. A method of producing a B6 vitamer comprising culturing a microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic gene under conditions such that the B6 vitamer is produced.

51. The method of claim 50, wherein the microorganism overexpresses at least one *Bacillus subtilis* B6 vitamer biosynthetic enzyme.

52. The method of claim 50, wherein the B6 vitamer is pyridoxine.

53. The method of claim 50, wherein the B6 vitamer is pyridoxal.

54. The method of claim 50, wherein the B6 vitamer is pyridoxamine.

55. The method of claim 50, wherein the microorganism overexpresses at least two B6 vitamer biosynthetic enzymes.

56. The method of claim 50, wherein the microorganism is Gram positive.

57. The method of claim 50, wherein the microorganism is Gram negative.

58. The method of claim 50, wherein the microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Cornyebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.

59. The method of claim 50, wherein the microorganism is of the genus *Bacillus*.

60. The method of claim 50, wherein the microorganism is *Bacillus subtilis*.

61. The method of claim 50, further comprising recovering the B6 vitamer.

62. A recombinant microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic gene.

63. A recombinant microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic enzyme.

64. The method of claim 63, wherein said enzyme is YaaD or YaaE.

65. The recombinant microorganism of claim 62 that overexpresses at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.

66. The recombinant microorganism of claim 62, wherein the B6 vitamer biosynthetic gene is selected from the group consisting of *yaaD* and *yaaE*.

67. The recombinant microorganism of claim 62, that is Gram positive.

68. The recombinant microorganism of claim 62, belonging to a genus selected from the group consisting of *Bacillus*, *Cornyebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.

69. The recombinant microorganism of claim 62 belonging to the genus *Bacillus*.

70. The recombinant microorganism of claim 62 which is *Bacillus subtilis*.

71. A recombinant microorganism selected from the group consisting of PX14 and PX17.

72. A vector comprising a nucleic acid sequence that encodes at least one *Bacillus* B6 vitamer biosynthetic gene operably linked to regulatory sequences.

73. The vector of claim 72, comprising a nucleic acid sequence that encodes at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.

74. The vector of claim 72, wherein the regulatory sequences comprise a constitutively active promoter.

75. The vector of claim 72, wherein the constitutively active promoter comprises P_{15} (SEQ ID NO:9) or P_{26} (SEQ ID NO:10) sequences.

76. The vector of claim 72, wherein the regulatory sequences comprise at least one artificial ribosome binding site (RBS).

77. A vector selected from the group consisting of pDX14R and pDX17R.

78. A recombinant microorganism comprising the vector of claim 72.

79. An isolated nucleic acid molecule that encodes at least one *Bacillus* B6 vitamer biosynthetic gene.

80. The isolated nucleic acid molecule of claim 79 that encodes at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.

81. An isolated *Bacillus* B6 vitamer biosynthetic enzyme polypeptide.

82. An isolated *Bacillus subtilis* B6 vitamer biosynthetic enzyme polypeptide.